

SEQUENCE LISTING

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<110> von der Osten, Claus
      Olsen, Arne Agerlin
      Roggen, Erwin Ludo

<120> A Modified Polypeptide

<130> 4923.204-US

<140> 09/024,532
<141> 1998-02-17

<150> PCT/DK98/00046
<151> 1998-02-06

<150> 0135/97
<151> 1997-02-06

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<170> FastSEQ for Windows Version 3.0

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<212> DNA
<213> bacillus sp.

<220>
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<222> (1)...(840)

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aac acc tca acc cct gct gcc tgg gat gta acc cgt gga agc agc act      96
Asn Thr Ser Thr Pro Ala Ala Trp Asp Val Thr Arg Gly Ser Ser Thr
 20          25          30

caa acg gtg gcg gtc ctt gat tcc gga gtg gat tat aac cac cct gat      144
Gln Thr Val Ala Val Leu Asp Ser Gly Val Asp Tyr Asn His Pro Asp
 35          40          45

ctt gca aga aaa gta ata aaa ggg tac gac ttt atc gac agg gac aat      192
Leu Ala Arg Lys Val Ile Lys Gly Tyr Asp Phe Ile Asp Arg Asp Asn
 50          55          60

aac cca atg gat ctt aac gga cat ggt acc cat gtt gcc ggt act gtt      240
Asn Pro Met Asp Leu Asn Gly His Gly Thr His Val Ala Gly Thr Val
 65          70          75          80

gct gct gat acg aac aat gga att ggc gta gcc ggt atg gca cca gat      288
Ala Ala Asp Thr Asn Asn Gly Ile Gly Val Ala Gly Met Ala Pro Asp
 85          90          95

acg aag atc ctt gcc gta cggt gtc ctt gat gcc aat gga agt ggc tca      336
Thr Lys Ile Leu Ala Val Arg Val Leu Asp Ala Asn Gly Ser Gly Ser
100         105         110

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ctt gac agc att gcc tca ggt atc cgc tat gct gct gat caa	ggg gca	384
Leu Asp Ser Ile Ala Ser Gly Ile Arg Tyr Ala Ala Asp Gln Gly Ala		
115	120	125
aag gta ctc aac ctc tcc ctt ggt tgc gaa tgc aac tcc aca act ctt		432

Lys Val Leu Asn Leu Ser Leu Gly Cys Glu Cys Asn Ser Thr Thr Leu			
130	135	140	
aag agt gcc gtc gac tat gca tgg aac aaa gga gct gta gtc gtt gct			480
Lys Ser Ala Val Asp Tyr Ala Trp Asn Lys Gly Ala Val Val Val Ala			
145	150	155	160
gct gca ggg aat gac aat gta tcc cgt aca ttc caa cca gct tct tac			528
Ala Ala Gly Asn Asp Asn Val Ser Arg Thr Phe Gln Pro Ala Ser Tyr			
165	170	175	
cct aat gcc att gca gta ggt gcc att gac tcc aat gat cga aaa gca			576
Pro Asn Ala Ile Ala Val Gly Ala Ile Asp Ser Asn Asp Arg Lys Ala			
180	185	190	
tca ttc tcc aat tac gga acg tgg gtg gat gtc act gct cca ggt gtg			624
Ser Phe Ser Asn Tyr Gly Thr Trp Val Asp Val Thr Ala Pro Gly Val			
195	200	205	
aac ata gca tca acc gtt ccg aat aat ggc tac tcc tac atg tct ggt			672
Asn Ile Ala Ser Thr Val Pro Asn Asn Gly Tyr Ser Tyr Met Ser Gly			
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acg tcc atg gca tcc cct cac gtg gcc ggt ttg gct gct ttg ttg gca			720
Thr Ser Met Ala Ser Pro His Val Ala Gly Leu Ala Ala Leu Leu Ala			
225	230	235	240
agt caa ggt aag aat aac gta caa atc cgc cag gcc att gag caa acc			768
Ser Gln Gly Lys Asn Asn Val Gln Ile Arg Gln Ala Ile Glu Gln Thr			
245	250	255	
gcc gat aag atc tct ggc act gga aca aac ttc aag tat ggt aaa atc			816
Ala Asp Lys Ile Ser Gly Thr Gly Thr Asn Phe Lys Tyr Gly Lys Ile			
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20 25 30			
Gln Thr Val Ala Val Leu Asp Ser Gly Val Asp Tyr Asn His Pro Asp			
35 40 45			
Leu Ala Arg Lys Val Ile Lys Gly Tyr Asp Phe Ile Asp Arg Asp Asn			
50 55 60			
Asn Pro Met Asp Leu Asn His Gly Thr His Val Ala Gly Thr Val			
65 70 75 80			
Ala Ala Asp Thr Asn Asn Gly Ile Gly Val Ala Gly Met Ala Pro Asp			
85 90 95			
Thr Lys Ile Leu Ala Val Arg Val Leu Asp Ala Asn Gly Ser Gly Ser			
100 105 110			
Leu Asp Ser Ile Ala Ser Gly Ile Arg Tyr Ala Ala Asp Gln Gly Ala			
115 120 125			
Lys Val Leu Asn Leu Ser Leu Gly Cys Glu Cys Asn Ser Thr Thr Leu			

130	135	140
Lys Ser Ala Val Asp Tyr Ala Trp Asn Lys Gly Ala Val Val Val Ala		
145	150	155
Ala Ala Gly Asn Asp Asn Val Ser Arg Thr Phe Gln Pro Ala Ser Tyr		160
165	170	175
Pro Asn Ala Ile Ala Val Gly Ala Ile Asp Ser Asn Asp Arg Lys Ala		
180	185	190
Ser Phe Ser Asn Tyr Gly Thr Trp Val Asp Val Thr Ala Pro Gly Val		
195	200	205
Asn Ile Ala Ser Thr Val Pro Asn Asn Gly Tyr Ser Tyr Met Ser Gly		
210	215	220
Thr Ser Met Ala Ser Pro His Val Ala Gly Leu Ala Ala Leu Leu Ala		
225	230	235
Ser Gln Gly Lys Asn Asn Val Gln Ile Arg Gln Ala Ile Glu Gln Thr		240
245	250	255
Ala Asp Lys Ile Ser Gly Thr Gly Thr Asn Phe Lys Tyr Gly Lys Ile		
260	265	270
Asn Ser Asn Lys Ala Val Arg Tyr		
275	280	

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 <212> PRT
 <213> Bacillus lentus

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Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser				
35	40		45	
Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr				
50	55		60	
His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu				
65	70		75	80
Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala				
85	90			95
Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala				
100	105			110
Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser				
115	120			125
Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly				
130	135		140	
Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser				
145	150		155	160
Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln				
165	170			175
Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile				
180	185		190	
Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr				
195	200		205	
Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala				
210	215		220	
Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile				
225	230		235	240
Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu				
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Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg				
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<212> PRT
<213> Arthromyces ramosus

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35 40 45
Lys Ile Leu Arg Ile Val Phe His Asp Ala Ile Gly Phe Ser Pro Ala
50 55 60
Leu Thr Ala Ala Gly Gln Phe Gly Gly Gly Ala Asp Gly Ser Ile
65 70 75 80
Ile Ala His Ser Asn Ile Glu Leu Ala Phe Pro Ala Asn Gly Gly Leu
85 90 95
Thr Asp Thr Ile Glu Ala Leu Arg Ala Val Gly Ile Asn His Gly Val
100 105 110
Ser Phe Gly Asp Leu Ile Gln Phe Ala Thr Ala Val Gly Met Ser Asn
115 120 125
Cys Pro Gly Ser Pro Arg Leu Glu Phe Leu Thr Gly Arg Ser Asn Ser
130 135 140
Ser Gln Pro Ser Pro Ser Leu Ile Pro Gly Pro Gly Asn Thr Val
145 150 155 160
Thr Ala Ile Leu Asp Arg Met Gly Asp Ala Gly Phe Ser Pro Asp Glu
165 170 175
Val Val Asp Leu Leu Ala Ala His Ser Leu Ala Ser Gln Glu Gly Leu
180 185 190
Asn Ser Ala Ile Phe Arg Ser Pro Leu Asp Ser Thr Pro Gln Val Phe
195 200 205
Asp Thr Gln Phe Tyr Ile Glu Thr Leu Leu Lys Gly Thr Thr Gln Pro
210 215 220
Gly Pro Ser Leu Gly Phe Ala Glu Glu Leu Ser Pro Phe Pro Gly Glu
225 230 235 240
Phe Arg Met Arg Ser Asp Ala Leu Leu Ala Arg Asp Ser Arg Thr Ala
245 250 255
Cys Arg Trp Gln Ser Met Thr Ser Ser Asn Glu Val Met Gly Gln Arg
260 265 270
Tyr Arg Ala Ala Met Ala Lys Met Ser Val Leu Gly Phe Asp Arg Asn
275 280 285
Ala Leu Thr Asp Cys Ser Asp Val Ile Pro Ser Ala Val Ser Asn Asn
290 295 300
Ala Ala Pro Val Ile Pro Gly Gly Leu Thr Val Asp Asp Ile Glu Val
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Ser Cys Pro Ser Glu Pro Phe Pro Glu Ile Ala Thr Ala Ser Gly Pro
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Leu Pro Ser Leu Ala Pro Ala Pro
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Glu Tyr Trp Ile Lys Ser Gly Thr Leu Val Pro Val Thr Arg Asn Asp				
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atc gtg aag ata gaa ggc atc gat gcc acc ggc ggc aat aac cag cct			816	
Ile Val Lys Ile Glu Gly Ile Asp Ala Thr Gly Gly Asn Asn Gln Pro				
235	240	245	250	
aac att ccg gat atc cct gcg cac cta tgg tac ttc ggg tta att ggg			864	
Asn Ile Pro Asp Ile Pro Ala His Leu Trp Tyr Phe Gly Leu Ile Gly				
255	260	265		
aca tgt ctt tag			876	
Thr Cys Leu *				

<210> 6
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 <213> Humicola lanuginosa DSM 4109

<220>
 <221> SIGNAL
 <222> (1)...(22)

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-5	1	5	10
Asn Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Gly Lys Asn Asn			
15	20	25	
Asp Ala Pro Ala Gly Thr Asn Ile Thr Cys Thr Gly Asn Ala Cys Pro			
30	35	40	
Glu Val Glu Lys Ala Asp Ala Thr Phe Leu Tyr Ser Phe Glu Asp Ser			
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Gly Val Gly Asp Val Thr Gly Phe Leu Ala Leu Asp Asn Thr Asn Lys			
60	65	70	
Leu Ile Val Leu Ser Phe Arg Gly Ser Arg Ser Ile Glu Asn Trp Ile			
75	80	85	90
Gly Asn Leu Asn Phe Asp Leu Lys Glu Ile Asn Asp Ile Cys Ser Gly			
95	100	105	
Cys Arg Gly His Asp Gly Phe Thr Ser Ser Trp Arg Ser Val Ala Asp			
110	115	120	
Thr Leu Arg Gln Lys Val Glu Asp Ala Val Arg Glu His Pro Asp Tyr			
125	130	135	
Arg Val Val Phe Thr Gly His Ser Leu Gly Gly Ala Leu Ala Thr Val			
140	145	150	
Ala Gly Ala Asp Leu Arg Gly Asn Gly Tyr Asp Ile Asp Val Phe Ser			
155	160	165	170
Tyr Gly Ala Pro Arg Val Gly Asn Arg Ala Phe Ala Glu Phe Leu Thr			
175	180	185	
Val Gln Thr Gly Gly Thr Leu Tyr Arg Ile Thr His Thr Asn Asp Ile			
190	195	200	
Val Pro Arg Leu Pro Pro Arg Glu Phe Gly Tyr Ser His Ser Ser Pro			
205	210	215	
Glu Tyr Trp Ile Lys Ser Gly Thr Leu Val Pro Val Thr Arg Asn Asp			
220	225	230	
Ile Val Lys Ile Glu Gly Ile Asp Ala Thr Gly Gly Asn Asn Gln Pro			
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Asn Ile Pro Asp Ile Pro Ala His Leu Trp Tyr Phe Gly Leu Ile Gly			
255	260	265	
Thr Cys Leu			

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